



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 20, 2022 – 04:05 PM EDT

PDB ID : 7SD5
Title : Crystallographic structure of neutralizing antibody 10-40 in complex with SARS-CoV-2 spike receptor binding domain
Authors : Reddem, E.R.; Casner, R.G.; Shapiro, L.
Deposited on : 2021-09-29
Resolution : 1.53 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.27
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.27

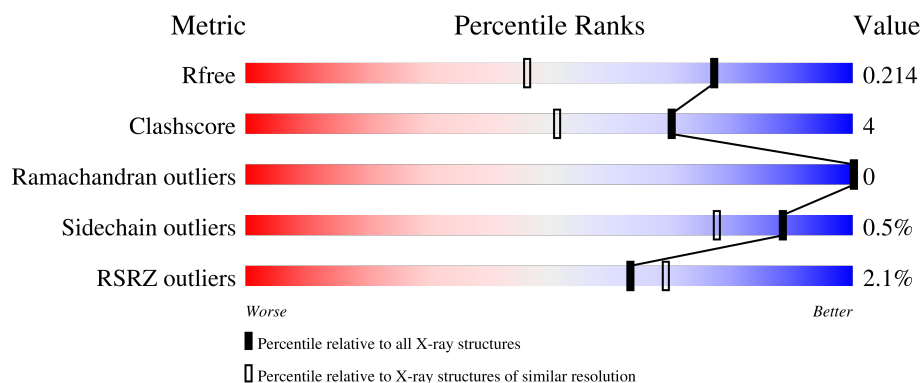
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.53 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2556 (1.56-1.52)
Clashscore	141614	2634 (1.56-1.52)
Ramachandran outliers	138981	2580 (1.56-1.52)
Sidechain outliers	138945	2577 (1.56-1.52)
RSRZ outliers	127900	2524 (1.56-1.52)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	239	<div> <div>%</div> <div> <div></div> <div>73%</div> <div>8%</div> <div>19%</div> </div> </div>
2	H	236	<div> <div>3%</div> <div> <div></div> <div>88%</div> <div>8%</div> <div>.</div> </div> </div>
3	L	216	<div> <div>%</div> <div> <div></div> <div>93%</div> <div>6%</div> <div>.</div> </div> </div>
4	B	2	<div> <div>100%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5628 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	193	Total	C	N	O	S	0	6	0
			1567	1004	263	292	8			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	316	ALA	-	expression tag	UNP P0DTC2
A	317	PRO	-	expression tag	UNP P0DTC2
A	318	ARG	-	expression tag	UNP P0DTC2
A	538	GLY	-	expression tag	UNP P0DTC2
A	539	SER	-	expression tag	UNP P0DTC2
A	540	LEU	-	expression tag	UNP P0DTC2
A	541	GLU	-	expression tag	UNP P0DTC2
A	542	VAL	-	expression tag	UNP P0DTC2
A	543	LEU	-	expression tag	UNP P0DTC2
A	544	PHE	-	expression tag	UNP P0DTC2
A	545	GLN	-	expression tag	UNP P0DTC2
A	546	GLY	-	expression tag	UNP P0DTC2
A	547	PRO	-	expression tag	UNP P0DTC2
A	548	GLY	-	expression tag	UNP P0DTC2
A	549	HIS	-	expression tag	UNP P0DTC2
A	550	HIS	-	expression tag	UNP P0DTC2
A	551	HIS	-	expression tag	UNP P0DTC2
A	552	HIS	-	expression tag	UNP P0DTC2
A	553	HIS	-	expression tag	UNP P0DTC2
A	554	HIS	-	expression tag	UNP P0DTC2

- Molecule 2 is a protein called 10-40 Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	227	Total	C	N	O	S	0	3	0
			1731	1103	282	340	6			

- Molecule 3 is a protein called 10-40 Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	213	Total	C	N	O	S	0	2	0
			1624	1009	272	337	6			

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	B	2	Total	C	N	O	0	0	0
			28	16	2	10			

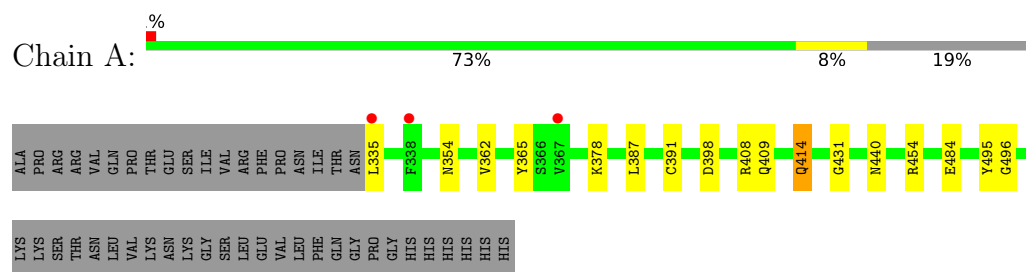
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	184	Total	O	0	0
			184	184		
5	H	275	Total	O	0	0
			275	275		
5	L	219	Total	O	0	0
			219	219		

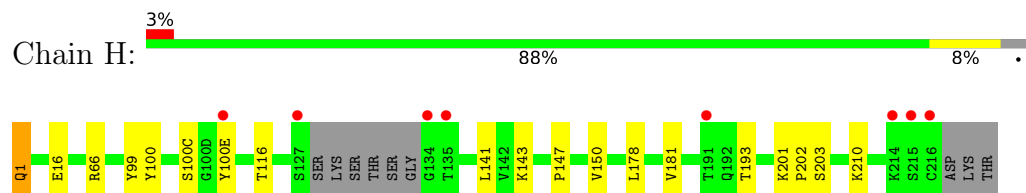
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

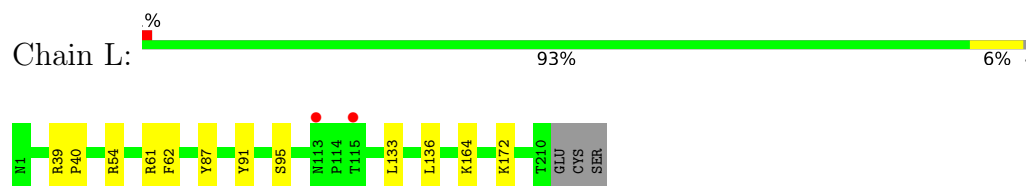
- Molecule 1: Spike protein S1



- Molecule 2: 10-40 Heavy chain



- Molecule 3: 10-40 Light chain



- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	75.76Å 79.84Å 118.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.44 – 1.53 49.88 – 1.50	Depositor EDS
% Data completeness (in resolution range)	96.8 (59.44-1.53) 96.8 (49.88-1.50)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.06 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.176 , 0.206 0.185 , 0.214	Depositor DCC
R_{free} test set	5520 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	25.9	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 42.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5628	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.71% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.74	1/1617 (0.1%)	0.89	3/2199 (0.1%)
2	H	0.82	1/1784 (0.1%)	0.96	1/2437 (0.0%)
3	L	0.79	0/1668	0.96	3/2275 (0.1%)
All	All	0.79	2/5069 (0.0%)	0.94	7/6911 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	16	GLU	CD-OE1	11.69	1.38	1.25
1	A	484	GLU	CD-OE1	9.20	1.35	1.25

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	66	ARG	NE-CZ-NH1	7.58	124.09	120.30
1	A	454	ARG	NE-CZ-NH2	-6.24	117.18	120.30
3	L	61	ARG	CG-CD-NE	-5.98	99.24	111.80
3	L	87	TYR	CB-CG-CD2	5.30	124.18	121.00
1	A	414[A]	GLN	CB-CA-C	5.20	120.81	110.40
1	A	414[B]	GLN	CB-CA-C	5.20	120.81	110.40
3	L	91	TYR	CB-CG-CD2	5.16	124.10	121.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1567	0	1486	14	0
2	H	1731	0	1696	17	0
3	L	1624	0	1553	8	0
4	B	28	0	25	0	0
5	A	184	0	0	2	0
5	H	275	0	0	2	1
5	L	219	0	0	2	0
All	All	5628	0	4760	35	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (35) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:1:GLN:HA	2:H:1:GLN:OE1	1.58	1.04
2:H:100(C):SER:HG	2:H:100(E)[B]:TYR:HD2	1.11	0.87
1:A:409:GLN:HA	1:A:414[B]:GLN:CG	2.04	0.86
1:A:409:GLN:HA	1:A:414[B]:GLN:HG3	1.60	0.84
2:H:1:GLN:N	5:H:301:HOH:O	2.11	0.82
2:H:100(C):SER:OG	2:H:100(E)[B]:TYR:HD2	1.64	0.80
1:A:414[B]:GLN:NE2	5:A:602:HOH:O	2.23	0.71
1:A:409:GLN:HA	1:A:414[B]:GLN:HG2	1.73	0.69
2:H:193:THR:HG23	2:H:210:LYS:HE3	1.78	0.65
2:H:150:VAL:HG23	2:H:178:LEU:HD21	1.83	0.61
2:H:150:VAL:CG2	2:H:178:LEU:HD21	2.34	0.57
3:L:172:LYS:NZ	5:L:302:HOH:O	2.26	0.57
1:A:335:LEU:HD23	1:A:362:VAL:O	2.03	0.57
2:H:181:VAL:HG21	3:L:136:LEU:CD1	2.38	0.54
1:A:408[B]:ARG:O	1:A:414[B]:GLN:HG2	2.08	0.54
3:L:95:SER:OG	5:L:301:HOH:O	2.18	0.51
1:A:440[B]:ASN:OD1	5:A:601:HOH:O	2.19	0.49
1:A:365:TYR:CD2	1:A:387:LEU:HB3	2.48	0.48
3:L:133:LEU:HD12	3:L:133:LEU:N	2.29	0.48
2:H:141:LEU:HG	2:H:143:LYS:HG3	1.96	0.47
1:A:354:ASN:O	1:A:398:ASP:HA	2.15	0.47
2:H:116[A]:THR:HG21	2:H:203:SER:HA	1.97	0.47
1:A:408[B]:ARG:NH1	3:L:54:ARG:H	2.13	0.46
3:L:54:ARG:HD3	3:L:62:PHE:O	2.16	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:391:CYS:HB3	1:A:522:ALA:HB1	1.98	0.46
2:H:100:TYR:HA	2:H:100(E)[A]:TYR:O	2.16	0.45
1:A:495:TYR:O	1:A:496:GLY:C	2.52	0.45
2:H:201:LYS:N	2:H:202:PRO:CD	2.80	0.45
2:H:1:GLN:OE1	2:H:1:GLN:CA	2.45	0.44
1:A:431:GLY:HA2	1:A:515:PHE:CD2	2.53	0.43
3:L:39:ARG:HB3	3:L:40:PRO:HD2	2.00	0.43
2:H:116[A]:THR:HG21	5:H:315:HOH:O	2.18	0.42
2:H:181:VAL:HG21	3:L:136:LEU:HD12	2.02	0.42
2:H:178:LEU:C	2:H:178:LEU:HD12	2.40	0.41
1:A:378[B]:LYS:HE3	2:H:99:TYR:CE2	2.56	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:H:350:HOH:O	5:H:502:HOH:O[3_544]	1.86	0.34

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	196/239 (82%)	192 (98%)	4 (2%)	0	100	100
2	H	226/236 (96%)	222 (98%)	4 (2%)	0	100	100
3	L	213/216 (99%)	207 (97%)	6 (3%)	0	100	100
All	All	635/691 (92%)	621 (98%)	14 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	171/208 (82%)	171 (100%)	0	100	100
2	H	199/204 (98%)	197 (99%)	2 (1%)	76	55
3	L	188/189 (100%)	187 (100%)	1 (0%)	88	77
All	All	558/601 (93%)	555 (100%)	3 (0%)	88	77

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	1	GLN
2	H	147	PRO
3	L	164	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	450	ASN
2	H	171	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

2 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	B	1	4,1	14,14,15	0.70	0	17,19,21	1.25	2 (11%)
4	NAG	B	2	4	14,14,15	0.44	0	17,19,21	1.51	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	B	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	B	2	4	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	2	NAG	C1-O5-C5	5.57	119.73	112.19
4	B	1	NAG	O5-C5-C6	2.40	110.97	107.20
4	B	1	NAG	C3-C4-C5	-2.27	106.19	110.24

There are no chirality outliers.

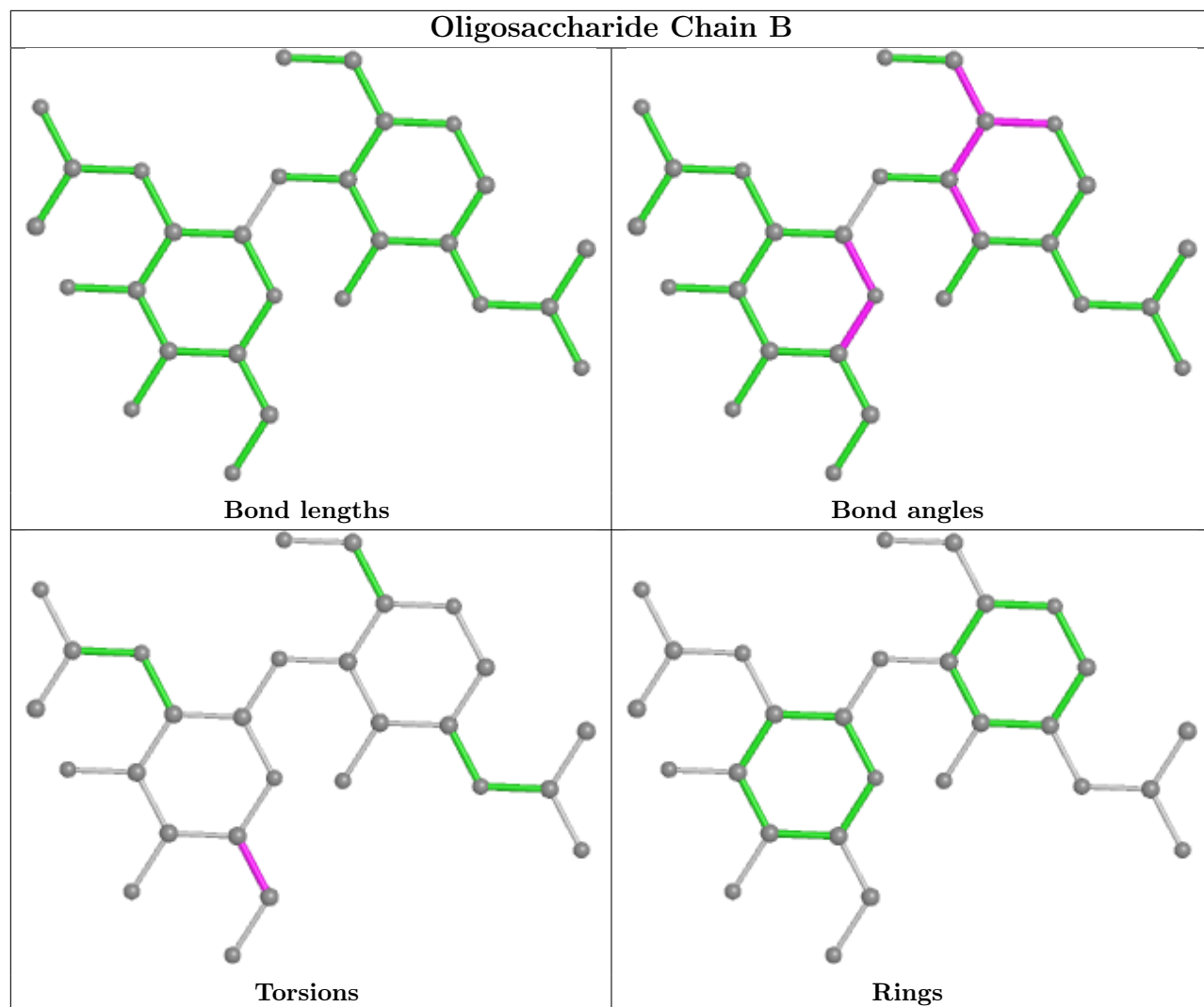
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	2	NAG	C4-C5-C6-O6
4	B	2	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	193/239 (80%)	-0.05	3 (1%) 72 77	20, 30, 49, 64	0
2	H	227/236 (96%)	0.12	8 (3%) 44 50	18, 25, 50, 90	0
3	L	213/216 (98%)	0.05	2 (0%) 84 86	18, 28, 48, 53	0
All	All	633/691 (91%)	0.04	13 (2%) 63 69	18, 28, 49, 90	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	216	CYS	4.8
2	H	134	GLY	3.3
1	A	335	LEU	3.2
2	H	191	THR	3.1
1	A	367	VAL	3.0
2	H	215	SER	3.0
2	H	127	SER	2.9
3	L	113	ASN	2.8
3	L	115	THR	2.5
2	H	135	THR	2.4
2	H	100(E)[A]	TYR	2.4
2	H	214	LYS	2.1
1	A	338	PHE	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

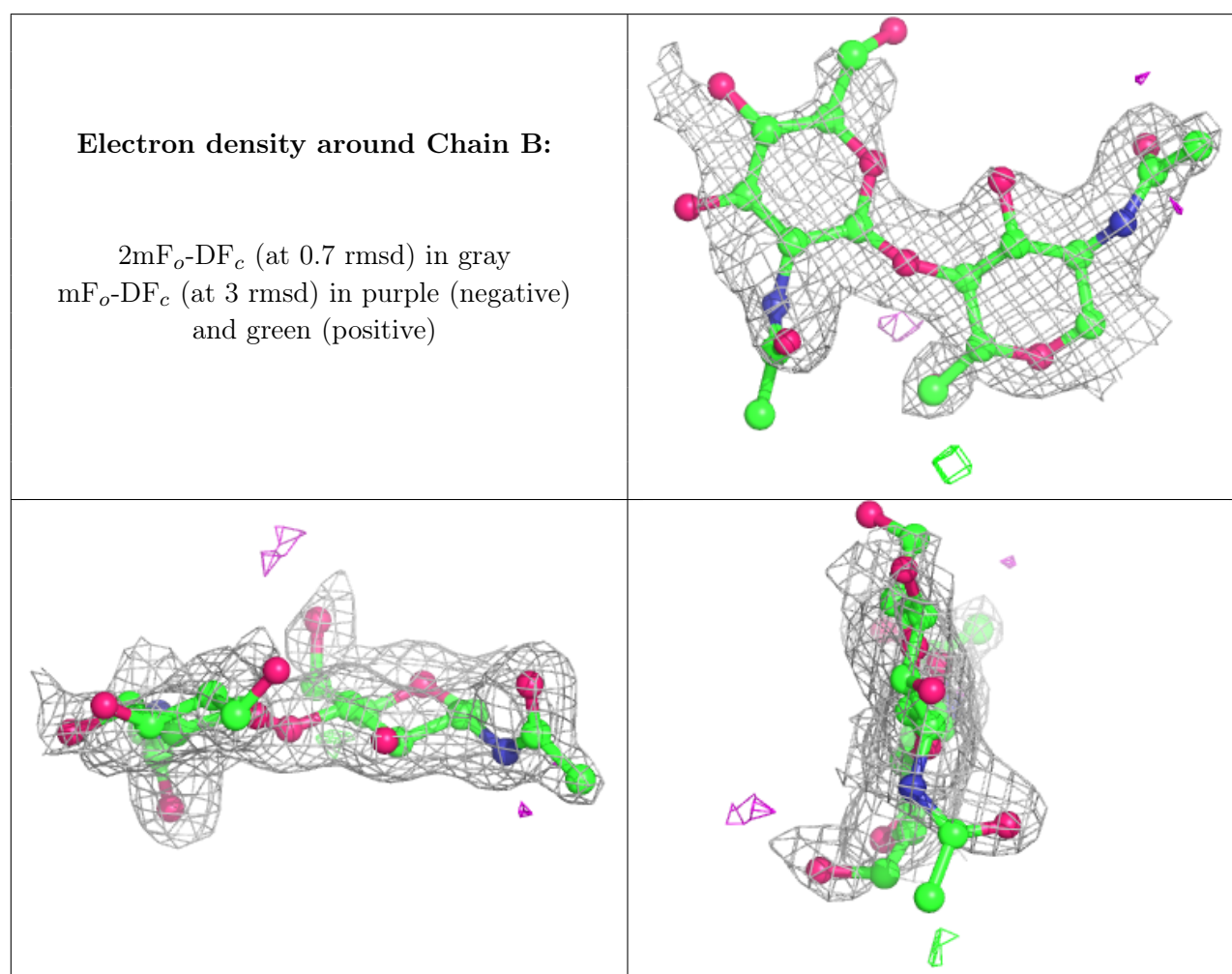
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	B	2	14/15	0.76	0.33	86,97,102,105	0
4	NAG	B	1	14/15	0.90	0.23	45,51,65,66	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.